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RAW SEQUENCE LISTING

DATE: 01/23/2003

PATENT APPLICATION: US/10/058,518

TIME: 10:32:01

Input Set : A:\06501-097001.txt

Output Set: N:\CRF4\01232003\J058518.raw

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4 <110> APPLICANT: Ota, Toshio
5      Isogai, Takao
6      Nishikawa, Tetsuo
7      Hayashi, Koji
8      Otsuka, Kaoru
9      Yamamoto, Jun-ichi
10     Ishii, Shizuko
11     Sugiyama, Tomoyasu
12     Wakamatsu, Ai
13     Nagai, Keiichi
14     Otsuki, Tetsuji
15     Funahashi, Shin-ichi
16     Miyata, Shoji
18 <120> TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH THE
19     MAINTENANCE OF DIFFERENTIATION OF SMOOTH MUSCLE CELLS
21 <130> FILE REFERENCE: 06501-097001
23 <140> CURRENT APPLICATION NUMBER: US 10/058,518
24 <141> CURRENT FILING DATE: 2002-01-28
26 <150> PRIOR APPLICATION NUMBER: PCT/JP00/05059
27 <151> PRIOR FILING DATE: 2000-07-28
29 <150> PRIOR APPLICATION NUMBER: US 60/183,322
30 <151> PRIOR FILING DATE: 2000-02-17
32 <150> PRIOR APPLICATION NUMBER: US 60/159,590
33 <151> PRIOR FILING DATE: 1999-10-18
35 <150> PRIOR APPLICATION NUMBER: JP 11-248036
36 <151> PRIOR FILING DATE: 1999-07-29
38 <150> PRIOR APPLICATION NUMBER: JP 2000-118776
39 <151> PRIOR FILING DATE: 2000-01-11
41 <150> PRIOR APPLICATION NUMBER: JP 2000-183767
42 <151> PRIOR FILING DATE: 2000-05-02
44 <160> NUMBER OF SEQ ID NOS: 16
46 <170> SOFTWARE: FastSEQ for Windows Version 4.0
48 <210> SEQ ID NO: 1
49 <211> LENGTH: 2256
50 <212> TYPE: DNA
51 <213> ORGANISM: Homo sapiens
53 <220> FEATURE:
54 <221> NAME/KEY: CDS
55 <222> LOCATION: (125)...(1366)
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59 gagttcctga gcgagtgagc ccggcagcgg gcgatagggg ggccaggtgc ctccacagtc      120
60 agcc atg gca gcg ctg cgc tac gcg ggg ctg gac gac acg gac agt gag      169

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61	Met	Ala	Ala	Leu	Arg	Tyr	Ala	Gly	Leu	Asp	Asp	Thr	Asp	Ser	Glu	
62	1				5					10					15	
64	gac	gag	ctg	cct	ccg	ggc	tgg	gag	gag	aga	acc	acc	aag	gac	ggc	tgg
65	Asp	Glu	Leu	Pro	Pro	Gly	Trp	Glu	Glu	Arg	Thr	Thr	Lys	Asp	Gly	Trp
66				20				25					30			
68	gtt	tac	tac	gcc	aat	cac	acc	gag	gag	aag	act	cag	tgg	gaa	cat	cca
69	Val	Tyr	Tyr	Ala	Asn	His	Thr	Glu	Glu	Lys	Thr	Gln	Trp	Glu	His	Pro
70				35				40					45			
72	aaa	act	gga	aaa	aga	aaa	cga	gtg	gca	gga	gat	ttg	cca	tac	gga	tgg
73	Lys	Thr	Gly	Lys	Arg	Lys	Arg	Val	Ala	Gly	Asp	Leu	Pro	Tyr	Gly	Trp
74			50					55				60				
76	gaa	caa	gaa	act	gat	gag	aac	gga	caa	gtg	ttt	ttt	gtt	gac	cat	ata
77	Glu	Gln	Glu	Thr	Asp	Glu	Asn	Gly	Gln	Val	Phe	Phe	Val	Asp	His	Ile
78		65					70				75					
80	aat	aaa	aga	acc	acc	tac	ttg	gac	cca	aga	ctg	gcg	ttt	act	gtg	gat
81	Asn	Lys	Arg	Thr	Thr	Tyr	Leu	Asp	Pro	Arg	Leu	Ala	Phe	Thr	Val	Asp
82	80				85				90				95			
84	gat	aat	ccg	acc	aag	cca	acc	acc	cgg	caa	aga	tac	gac	ggc	agc	acc
85	Asp	Asn	Pro	Thr	Lys	Pro	Thr	Thr	Arg	Gln	Arg	Tyr	Asp	Gly	Ser	Thr
86				100				105					110			
88	act	gcc	atg	gaa	att	ctc	cag	ggc	ccg	gat	ttc	act	ggc	aaa	gtg	gtt
89	Thr	Ala	Met	Glu	Ile	Leu	Gln	Gly	Pro	Asp	Phe	Thr	Gly	Lys	Val	Val
90				115				120					125			
92	gtg	gtc	act	gga	gct	aat	tca	gga	ata	ggg	ttc	gaa	acc	gcc	aag	tct
93	Val	Val	Thr	Gly	Ala	Asn	Ser	Gly	Ile	Gly	Phe	Glu	Thr	Ala	Lys	Ser
94			130					135				140				
96	ttt	gcc	ctc	cat	ggt	gca	cat	gtg	atc	ttg	gcc	tgc	agg	aac	atg	gca
97	Phe	Ala	Leu	His	Gly	Ala	His	Val	Ile	Leu	Ala	Cys	Arg	Asn	Met	Ala
98		145					150				155					
100	agg	gcg	agt	gaa	gca	gtg	tca	cgc	att	tta	gaa	gaa	tgg	cat	aaa	gcc
101	Arg	Ala	Ser	Glu	Ala	Val	Ser	Arg	Ile	Leu	Glu	Glu	Trp	His	Lys	Ala
102	160				165				170				175			
104	aag	gta	gaa	gca	atg	acc	ctg	gac	ctc	gct	ctg	ctc	cgt	agc	gtg	cag
105	Lys	Val	Glu	Ala	Met	Thr	Leu	Asp	Leu	Ala	Leu	Leu	Arg	Ser	Val	Gln
106				180				185				190				
108	cat	ttt	gct	gaa	gca	ttc	aag	gcc	aag	aat	gtg	cct	ctt	cat	gtg	ctt
109	His	Phe	Ala	Glu	Ala	Phe	Lys	Ala	Lys	Asn	Val	Pro	Leu	His	Val	Leu
110				195				200				205				
112	gtg	tgc	aac	gca	gca	act	ttt	gct	cta	ccc	tgg	agt	ctc	acc	aaa	gat
113	Val	Cys	Asn	Ala	Ala	Thr	Phe	Ala	Leu	Pro	Trp	Ser	Leu	Thr	Lys	Asp
114			210					215				220				
116	ggc	ctg	gag	acc	acc	ttt	caa	gtg	aat	cat	ctg	ggg	cac	ttc	tac	ctt
117	Gly	Leu	Glu	Thr	Thr	Phe	Gln	Val	Asn	His	Leu	Gly	His	Phe	Tyr	Leu
118		225					230				235					
120	gtc	cag	ctc	ctc	cag	gat	gtt	ttg	tgc	cgc	tca	gct	cct	gcc	cgt	gtc
121	Val	Gln	Leu	Leu	Gln	Asp	Val	Leu	Cys	Arg	Ser	Ala	Pro	Ala	Arg	Val
122	240				245				250			255				
124	att	gtg	gtc	tcc	tca	gag	tcc	cat	cga	ttt	aca	gat	att	aac	gac	tcc
125	Ile	Val	Val	Ser	Ser	Glu	Ser	His	Arg	Phe	Thr	Asp	Ile	Asn	Asp	Ser

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126          260          265          270
128 ttg gga aaa ctg gac ttc agt cgc ctc tct cca aca aaa aac gac tat      985
129 Leu Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr
130          275          280          285
132 tgg gcg atg ctg gct tat aac agg tcc aag ctc tgc aac atc ctc ttc      1033
133 Trp Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe
134          290          295          300
136 tcc aac gag ctg cac cgt cgc ctc tcc cca cgc ggg gtc acg tcg aac      1081
137 Ser Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn
138          305          310          315
140 gca gtg cat cct gga aat atg atg tac tcc aac att cat cgc agc tgg      1129
141 Ala Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp
142          320          325          330
144 tgg gtg tac aca ctg ctg ttt acc ttg gcg agg cct ttc acc aag tcc      1177
145 Trp Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser
146          340          345          350
148 atg caa cag gga gct gcc acc acc gtg tac tgt gct gct gtc cca gaa      1225
149 Met Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu
150          355          360          365
152 ctg gag ggt ctg gga ggg atg tac ttc aac aac tgc tgc cgc tgc atg      1273
153 Leu Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met
154          370          375          380
156 ccc tca cca gaa gct cag agc gaa gag acg gcc cgg acc ctg tgg gcg      1321
157 Pro Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala
158          385          390          395
160 ctc agc gag agg ctg atc caa gaa cgg ctt ggc agc cag tcc ggc      1366
161 Leu Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly
162          400          405          410
164 taagtggagc tcagagcgga tgggcacaca caccgcctt gtgtgtgtcc cctcacgcaa      1426
165 gtgccagggc tgggccctt ccaaatgtcc ctccaacaca gatccgcaag agtaaaggaa      1486
166 ataagagcag tcacaacaga gtgaaaaatc ttaagtacca atgggaagca gggaattcct      1546
167 ggggtaaaagt atcacttttc tggggctggg ctaggcatag gtctctttgc tttctggtgg      1606
168 tggcctgttt gaaagtaaaa acctgcttgg tgtgtaggtt ccgtatctcc ctggagaagc      1666
169 accagcaatt ctctttcttt tactgttata gaatagcctg aggtcccctc gtcccatcca      1726
170 gctaccacca cggccaccac tgcagccggg ggctggcctt ctctactta gggaagaaaa      1786
171 agcaagtgtt cactgtcctt tgctgcattg atccaggaga taattgtttc attcatcctg      1846
172 accaagactg agccagctta gcaactgctg gggagacaaa tctcagaacc ttgtcccagc      1906
173 cagtgaggat gacagtgaca ccagagggga gtagaatacg cagaactacc aggtggcaaa      1966
174 gtacttgtca tagactcctt tgctaatagct atgcaaaaaa ttcttttagag attataacaa      2026
175 atttttcaaaa tcatctcctta gataccttga aaggcaggaa gggaagcgta tataacttaag      2086
176 aatacacagg atattttggg gggcagagaa taaaacgtta gttaatccct ttgtctgtca      2146
177 atcacagtct cagttctctt gctttcacat tgtacttaaa cctcctgctg tgcctcgcat      2206
178 cctatgctta ataaaaaagaa atgcttgaat atcaaaaaaa aaaaaaaaac      2256
180 <210> SEQ ID NO: 2
181 <211> LENGTH: 414
182 <212> TYPE: PRT
183 <213> ORGANISM: Homo sapiens
185 <400> SEQUENCE: 2
186 Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu Asp

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187 1 5 10 15
188 Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp Val
189 20 25 30
190 Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys
191 35 40 45
192 Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu
193 50 55 60
194 Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn
195 65 70 75 80
196 Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp
197 85 90 95
198 Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr
199 100 105 110
200 Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val Val
201 115 120 125
202 Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe
203 130 135 140
204 Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala Arg
205 145 150 155 160
206 Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala Lys
207 165 170 175
208 Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln His
209 180 185 190
210 Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu Val
211 195 200 205
212 Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp Gly
213 210 215 220
214 Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu Val
215 225 230 235 240
216 Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val Ile
217 245 250 255
218 Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser Leu
219 260 265 270
220 Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr Trp
221 275 280 285
222 Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser
223 290 295 300
224 Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala
225 305 310 315 320
226 Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp Trp
227 325 330 335
228 Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser Met
229 340 345 350
230 Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu
231 355 360 365
232 Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro
233 370 375 380
234 Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu
235 385 390 395 400

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236 Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly
237           405           410
239 <210> SEQ ID NO: 3
240 <211> LENGTH: 251
241 <212> TYPE: DNA
242 <213> ORGANISM: Gallus gallus
244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (3)...(251)
248 <400> SEQUENCE: 3
249 ag gag cgc acc acc aag gac ggc tgg gtt tac tac gcc aat cac ttg      47
250   Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu
251     1           5           10           15
253 gaa gaa aaa aca cag tgg gaa cat cca aaa tct ggg aag agg aaa cgt      95
254 Glu Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg
255           20           25           30
257 gtt gca gga ggt ctg cca tat gga tgg gag cag gag act gat gaa aat      143
258 Val Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn
259           35           40           45
261 gga cag gtc tat ttt gta gac cac ata aac aaa aga act acc tat ctg      191
262 Gly Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu
263           50           55           60
265 gat cca aga ttg gcc ttt aca gtt gaa gat aat cca gca aag cca cct      239
266 Asp Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro
267     65           70           75
269 act aga caa aaa      251
270 Thr Arg Gln Lys
271 80
274 <210> SEQ ID NO: 4
275 <211> LENGTH: 83
276 <212> TYPE: PRT
277 <213> ORGANISM: Gallus gallus
279 <400> SEQUENCE: 4
280 Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu Glu
281 1           5           10           15
282 Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg Val
283           20           25           30
284 Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn Gly
285           35           40           45
286 Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu Asp
287     50           55           60
288 Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro Thr
289 65           70           75           80
290 Arg Gln Lys
292 <210> SEQ ID NO: 5
293 <211> LENGTH: 30
294 <212> TYPE: RNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:

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VERIFICATION SUMMARY

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